

1653

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/553,368

DATE: 05/09/2000  
TIME: 16:38:51

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\05092000\I553368.raw

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JUN-7 2000  
JTC 1600 MAIL ROOM

3 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Ill, Charles R. et al.  
7 (ii) TITLE OF INVENTION: NOVEL VECTORS AND GENES EXHIBITING  
8 INCREASED EXPRESSION  
10 (iii) NUMBER OF SEQUENCES: 11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
14 (B) STREET: 28 STATE STREET  
15 (C) CITY: BOSTON  
16 (D) STATE: MASSACHUSETTS  
17 (E) COUNTRY: US  
18 (F) ZIP: 02109  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
C--> 26 (vi) CURRENT APPLICATION DATA:  
C--> 27 (A) APPLICATION NUMBER: US/09/553,368  
C--> 28 (B) FILING DATE: 20-Apr-2000  
29 (C) CLASSIFICATION:  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: US 60/067,614  
33 (B) FILING DATE: 05 DECEMBER 1997  
34 (A) APPLICATION NUMBER: US 60/071,596  
35 (B) FILING DATE: 16 JANUARY 1998  
36 (A) APPLICATION NUMBER: 09/205,817  
37 (B) FILING DATE: 04 DECEMBER 1998  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: DOUROS, TIMOTHY J.  
41 (B) REGISTRATION NUMBER: 41,716  
42 (C) REFERENCE/DOCKET NUMBER: TTI-180DV  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: (617)227-7400  
46 (B) TELEFAX: (617)742-4214  
48 (2) INFORMATION FOR SEQ ID NO: 1:  
50 (i) SEQUENCE CHARACTERISTICS:  
51 (A) LENGTH: 4374 base pairs  
52 (B) TYPE: nucleic acid  
53 (C) STRANDEDNESS: single  
54 (D) TOPOLOGY: linear  
56 (ii) MOLECULE TYPE: cDNA  
58 (ix) FEATURE:  
59 (A) NAME/KEY: CDS  
60 (B) LOCATION: 1..4374  
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
64 ATG GAA ATA GAG CTC TCC ACC TGC TTC TTT CTG TGC CTT TTG CGA TTC

48

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65	Met	Glu	Ile	Glu	Leu	Ser	Thr	Cys	Phe	Phe	Leu	Cys	Leu	Leu	Arg	Phe	
66	1				5					10					15		
68	TGC	TTT	AGT	GCC	ACC	AGA	AGA	TAC	TAC	CTG	GGT	GCA	GTG	GAA	CTG	TCA	96
69	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser	
70				20					25					30			
72	TGG	GAC	TAT	ATG	CAA	AGT	GAT	CTC	GGA	GAG	CTG	CCT	GTG	GAC	GCA	AGA	144
73	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	
74				35					40					45			
76	TTT	CCT	CCT	CGC	GTG	CCA	AAA	TCT	TTT	CCA	TTC	AAC	ACC	TCA	GTC	GTG	192
77	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	
78				50					55					60			
80	TAC	AAA	AAG	ACT	CTG	TTT	GTA	GAA	TTC	ACG	GTT	CAC	CTT	TTC	AAC	ATC	240
81	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Val	His	Leu	Phe	Asn	Ile	
82	65					70				75					80		
84	GCT	AAG	CCA	AGG	CCA	CCC	TGG	ATG	GGT	CTG	CTA	GGT	CCT	ACC	ATC	CAA	288
85	Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln	
86					85					90					95		
88	GCT	GAG	GTT	TAT	GAT	ACA	GTG	GTC	ATT	ACA	CTT	AAG	AAC	ATG	GCT	TCC	336
89	Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser	
90				100					105					110			
92	CAT	CCT	GTC	TCC	CTT	CAT	GCT	GTT	GGT	GTA	TCC	TAC	TGG	AAA	GCT	TCT	384
93	His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser	
94				115					120					125			
96	GAG	GGA	GCT	GAA	TAT	GAT	GAT	CAG	ACC	AGT	CAA	AGG	GAG	AAA	GAA	GAT	432
97	Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	
98				130					135					140			
100	GAT	AAA	GTC	TTC	CCT	GGT	GGA	AGC	CAT	ACA	TAT	GTC	TGG	CAA	GTC	CTG	480
101	Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	
102	145					150						155			160		
104	AAA	GAG	AAT	GGT	CCA	ATG	GCC	TCC	GAC	CCA	CTG	TGC	CTT	ACC	TAC	TCA	528
105	Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	
106					165					170					175		
108	TAT	CTT	TCT	CAT	GTG	GAC	CTG	GTT	AAA	GAC	TTG	AAT	TCA	GGC	CTC	ATT	576
109	Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	
110				180					185					190			
112	GGA	GCC	CTA	CTA	GTA	TGT	AGA	GAA	GGG	AGT	CTG	GCC	AAG	GAA	AAG	ACA	624
113	Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	
114				195					200					205			
116	CAG	ACC	TTG	CAC	AAA	TTT	ATA	CTA	CTT	TTT	GCT	GTA	TTT	GAT	GAA	GGG	672
117	Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	
118				210					215					220			
120	AAA	AGT	TGG	CAC	TCA	GAA	ACA	AAG	AAC	TCC	CTC	ATG	CAA	GAT	AGG	GAT	720
121	Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	
122	225					230						235			240		
124	GCT	GCA	TCT	GCT	CGG	GCC	TGG	CCT	AAA	ATG	CAC	ACA	GTC	AAT	GGT	TAT	768
125	Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	
126					245					250					255		
128	GTA	AAC	AGG	AGC	CTG	CCA	GGA	CTG	ATT	GGA	TGC	CAC	AGG	AAA	TCA	GTC	816
129	Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	

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130		260		265		270	
132	TAT TGG CAT	GTT ATA GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA	864				
133	Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile						
134		275	280	285			
136	TTC CTC GAA GGA CAC ACA TTT CTT GTT AGA AAC CAT CGC CAG GCG TCC	912					
137	Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser						
138		290	295	300			
140	TTG GAA ATC TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC CTC ATG	960					
141	Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met						
142	305	310	315	320			
144	GAC CTT GGA CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT	1008					
145	Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His						
146		325	330	335			
148	GAT GGC ATG GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC	1056					
149	Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro						
150		340	345	350			
152	CAA CTA CGA ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT	1104					
153	Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp						
154		355	360	365			
156	CTT ACC GAT TCT GAA ATG GAT GTG GTC AGA TTT GAT GAT GAC AAC TCT	1152					
157	Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser						
158		370	375	380			
160	CCT TCC TTT ATC CAA ATT CGC TCA GTT GCC AAG AAG CAT CCT AAA ACT	1200					
161	Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr						
162	385	390	395	400			
164	TGG GTA CAT TAC ATT GCT GCT GAA GAG GAG GAC TGG GAC TAT GCT CCC	1248					
165	Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro						
166		405	410	415			
168	TTA GTC CTC GCC CCC GAT GAC AGA AGT TAT AAA AGT CAA TAT TTG AAC	1296					
169	Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn						
170		420	425	430			
172	AAT GGC CCT CAG CGG ATT GGA AGG AAG TAC AAA AAA GTC CGA TTT ATG	1344					
173	Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met						
174		435	440	445			
176	GCA TAC ACA GAT GAA ACC TTT AAG ACT CGT GAA GCT ATT CAG CAT GAA	1392					
177	Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu						
178		450	455	460			
180	TCA GGA ATC TTG GGA CCT TTA CTT TAT GGG GAA GTT GGA GAC ACA CTG	1440					
181	Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu						
182	465	470	475	480			
184	CTC ATT ATA TTT AAG AAT CAA GCA AGC AGA CCA TAT AAC ATC TAC CCT	1488					
185	Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro						
186		485	490	495			
188	CAC GGA ATC ACC GAT GTC CGT CCT TTG TAT TCA CGC AGA TTA CCA AAA	1536					
189	His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys						
190		500	505	510			
192	GGA GTA AAA CAT TTG AAG GAT TTT CCA ATT CTG CCC GGA GAA ATA TTC	1584					
193	Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe						
194		515	520	525			

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196	AAA	TAT	AAA	TGG	ACA	GTG	ACT	GTA	GAA	GAT	GGG	CCA	ACT	AAA	TCA	GAT	1632
197	Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	
198		530					535					540					
200	CCT	CGG	TGC	CTG	ACC	CGC	TAT	TAC	TCT	AGT	TTC	GTC	AAT	ATG	GAG	AGA	1680
201	Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	
202	545					550				555					560		
204	GAT	CTA	GCT	TCA	GGA	CTC	ATT	GGC	CCT	CTC	CTC	ATC	TGC	TAC	AAA	GAA	1728
205	Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	
206					565					570					575		
208	TCT	GTA	GAT	CAA	AGA	GGA	AAC	CAG	ATA	ATG	TCA	GAC	AAG	AGG	AAT	GTC	1776
209	Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	
210				580					585					590			
212	ATC	CTG	TTT	TCT	GTA	TTT	GAT	GAG	AAC	CGA	AGC	TGG	TAC	CTC	ACA	GAG	1824
213	Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	
214			595				600					605					
216	AAT	ATA	CAA	CGC	TTT	CTC	CCC	AAT	CCC	GCT	GGA	GTG	CAG	CTT	GAG	GAT	1872
217	Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	
218		610					615					620					
220	CCA	GAG	TTC	CAA	GCC	TCC	AAC	ATC	ATG	CAC	AGC	ATC	AAT	GGC	TAT	GTT	1920
221	Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	
222	625					630				635					640		
224	TTC	GAT	AGT	TTG	CAG	TTG	TCA	GTT	TGT	TTG	CAT	GAA	GTA	GCA	TAC	TGG	1968
225	Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	
226					645					650					655		
228	TAC	ATT	CTA	AGC	ATT	GGA	GCA	CAG	ACT	GAC	TTC	CTT	TCT	GTC	TTC	TTC	2016
229	Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	
230				660					665					670			
232	TCT	GGA	TAT	ACC	TTC	AAA	CAC	AAA	ATG	GTC	TAT	GAA	GAC	ACA	CTC	ACC	2064
233	Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	
234			675				680					685					
236	CTA	TTC	CCA	TTC	TCC	GGA	GAA	ACT	GTC	TTC	ATG	TCG	ATG	GAA	AAC	CCA	2112
237	Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	
238		690					695					700					
240	GGA	CTA	TGG	ATT	CTG	GGG	TGC	CAC	AAC	TCA	GAC	TTT	CGG	AAC	AGA	GGC	2160
241	Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	
242	705					710				715					720		
244	ATG	ACC	GCC	TTA	CTG	AAA	GTT	TCC	AGT	TGT	GAC	AAG	AAC	ACT	GGA	GAT	2208
245	Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	
246					725					730					735		
248	TAT	TAC	GAG	GAC	AGT	TAT	GAA	GAT	ATT	TCA	GCA	TAC	TTG	CTG	AGT	AAA	2256
249	Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	
250				740					745					750			
252	AAC	AAT	GCC	ATT	GAA	CCA	AGA	AGC	TTC	TCC	CAG	AAC	CCA	CCA	GTC	TTG	2304
253	Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Pro	Pro	Val	Leu	
254			755				760					765					
256	AAA	CGC	CAT	CAA	CGG	GAA	ATA	ACT	CGT	ACT	ACT	CTT	CAA	TCA	GAT	CAA	2352
257	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	
258		770					775					780					
260	GAG	GAA	ATT	GAC	TAT	GAT	GAT	ACC	ATA	TCA	GTT	GAA	ATG	AAG	AAG	GAA	2400

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261	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	
262	785					790					795					800	
264	GAT	TTC	GAC	ATT	TAT	GAT	GAG	GAT	GAA	AAT	CAG	AGC	CCC	CGC	AGC	TTT	2448
265	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	
266					805					810					815		
268	CAA	AAG	AAA	ACA	CGA	CAC	TAT	TTT	ATT	GCT	GCA	GTG	GAG	AGG	CTC	TGG	2496
269	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	
270				820						825				830			
272	GAT	TAT	GGG	ATG	AGT	AGC	TCC	CCA	CAT	GTT	CTA	AGA	AAC	AGG	GCT	CAG	2544
273	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	
274			835				840						845				
276	AGT	GGC	AGT	GTC	CCT	CAG	TTC	AAG	AAA	GTA	GTA	TTC	CAG	GAA	TTT	ACC	2592
277	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	
278		850					855					860					
280	GAT	GGC	TCC	TTT	ACT	CAA	CCC	TTA	TAC	CGT	GGA	GAA	CTA	AAT	GAA	CAT	2640
281	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	
282	865					870					875				880		
284	TTG	GGA	CTC	CTG	GGG	CCA	TAT	ATA	AGA	GCA	GAA	GTT	GAA	GAT	AAT	ATC	2688
285	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	
286				885						890					895		
288	ATG	GTT	ACC	TTC	AGA	AAT	CAG	GCC	TCT	CGT	CCC	TAT	TCC	TTC	TAT	TCT	2736
289	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	
290			900						905				910				
292	TCC	CTC	ATA	TCA	TAT	GAG	GAA	GAT	CAG	AGG	CAA	GGA	GCA	GAA	CCT	AGA	2784
293	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	
294			915				920					925					
296	AAA	AAC	TTT	GTC	AAG	CCT	AAT	GAA	ACC	AAA	ACT	TAC	TTT	TGG	AAA	GTG	2832
297	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	
298		930				935					940						
300	CAA	CAT	CAT	ATG	GCA	CCC	ACT	AAA	GAT	GAG	TTT	GAC	TGC	AAA	GCC	TGG	2880
301	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	
302	945				950						955				960		
304	GCT	TAT	TTC	TCC	GAT	GTC	GAC	CTG	GAA	AAA	GAT	GTG	CAC	TCA	GGC	CTG	2928
305	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	
306				965						970					975		
308	ATT	GGA	CCC	CTT	CTG	GTC	TGC	CAC	ACC	AAC	ACA	CTG	AAC	CCT	GCT	CAT	2976
309	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	
310			980						985				990				
312	GGG	AGA	CAA	GTG	ACA	GTA	CAG	GAA	TTT	GCT	CTG	TTT	TTC	ACC	ATC	TTC	3024
313	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	
314		995					1000					1005					
316	GAT	GAG	ACC	AAA	AGC	TGG	TAC	TTC	ACT	GAA	AAT	ATG	GAA	AGA	AAC	TGC	3072
317	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	
318		1010					1015					1020					
320	AGG	GCT	CCC	TGC	AAT	ATC	CAG	ATG	GAA	GAT	CCC	ACT	TTT	AAA	GAG	AAT	3120
321	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	
322	1025				1030					1035					1040		
324	TAT	CGC	TTC	CAT	GCA	ATC	AAT	GGC	TAC	ATA	ATG	GAT	ACA	CTA	CCT	GGC	3168
325	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	

## VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

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L:1319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1487 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:1491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3